IN THE CLAIMS:

Sub E1 1. (Amended four times) A pair of nucleic acid probes having comparable size, said size being selected from the group consisting of from 1 to 100 kb, from 1 to 10 kb, 7 to 15 kb, 10 to 20 kb, 10 to 30 kb, 20 to 40 kb, 30 to 50 kb, 40 to 60 kb, 50 to 70 kb, 60 to 80 kb, 70 to 90 kb, and 80 to 100 kb, and flanking a potential breakpoint in a single chromosome, each of said pair of probes being labeled with at least one different reporter molecule such that a split signal arises after a break within said potential breakpoint.

D1

2. (Amended four times) A pair of nucleic acid probes of comparable size, said size being selected from the group consisting of from 1 to 100 kb, from 1 to 10 kb, 7 to 15 kb, 10 to 20 kb, 10 to 30 kb, 20 to 40 kb, 30 to 50 kb, 40 to 60 kb, 50 to 70 kb, 60 to 80 kb, 70 to 90 kb, and 80 to 100 kb, and flanking a potential breakpoint in a single chromosome, which pair of nucleic acid probes hybridize to a nucleic acid molecule at a genomic distance of from about 50 kb to no more than 100 kb.

D2 Sub E2 4. (Amended four times) The pair of nucleic acid probes of claim 2, each of said pair of nucleic acid probes being labeled directly or indirectly with at least one reporter molecule.

D3 Sub E3 6. (Amended four times) The pair of nucleic acid probes of claim 5 wherein the pair of nucleic acid probes hybridize to a single corresponding nucleic acid molecule.

Sub E4 11. (Amended four times) A method of detecting a nucleic acid molecule having a chromosomal aberration, said method comprising:

D4 providing a pair of nucleic acid probes to analyze a sample believed to contain said nucleic acid, said pair of nucleic acid probes having comparable size, said size being selected from the group consisting of 1 to 100 kb, 1 to 10 kb, 7 to 15 kb, 10 to 20 kb, 10 to 30 kb, 20 to 40 kb, 30 to 50 kb, 40 to 60 kb, 50 to 70 kb, 60 to 80 kb, 70 to 90 kb and 80 to 100 kb, and said pair of nucleic acid probes flanking a potential breakpoint in a single chromosome, each of said pair of probes being labeled with at least one different reporter molecule;

hybridizing said pair of nucleic acid probes to said nucleic acid; and

detecting the presence of said at least one different reporter molecule.

12. (Amended) A method of detecting cells suspected of having a chromosomal aberration, said method comprising:

providing a pair of nucleic acid probes to analyze nucleic acid of said cells, said pair of nucleic acid probes having comparable size, said size being selected from the group consisting of 1 to 100 kb, 1 to 10 kb, 7 to 15 kb, 10 to 20 kb, 10 to 30 kb, 20 to 40 kb, 30 to 50 kb, 40 to 60 kb, 50 to 70 kb, 60 to 80 kb, 70 to 90 kb and 80 to 100 kb, and said pair of nucleic acid probes flanking a potential breakpoint in a single chromosome, each of said pair of nucleic acid probes being labeled with at least one different reporter molecule;

hybridizing said pair of nucleic acid probes to the nucleic acid of at least one of said cells; and

detecting the presence of said at least one different reporter molecule.

17. (Amended three times) The pair of nucleic acid probes of claim 1, wherein the pair of nucleic acid probes hybridize to a single corresponding nucleic acid molecule.

Please add the following new claims:

22. (New) A method of detecting a break within a potential breakpoint of a single chromosome, said method comprising:

associating a pair of nucleic acid probes and a sample believed to contain nucleic acid complementary to said pair of nucleic acid probes, said pair of nucleic acid probes having comparable size, said size being selected from the group consisting of 1 to 100 kb, 1 to 10 kb, 7 to 15 kb, 10 to 20 kb, 10 to 30 kb, 20 to 40 kb, 30 to 50 kb, 40 to 60 kb, 50 to 70 kb, 60 to 80 kb, 70 to 90 kb and 80 to 100 kb, each nucleic acid probe of said pair of nucleic acid probes being labeled with at least one different reporter molecule and flanking a potential breakpoint in said single chromosome;

hybridizing said pair of nucleic acid probes to said nucleic acid; and

determining whether a split-signal is present in said sample.

R1.126

~~22~~ 23. (New) The pair of nucleic acid probes of claim ~~21~~ 22, which pair of nucleic acid probes hybridize to a nucleic acid molecule at a genomic distance of from about 50 kb to no more than 100 kb.

R1.126

~~23~~ 24. (New) The pair of nucleic acid probes of claim ~~21~~ 22, wherein the at least one reporter molecule of said at least one different report molecule is selected from the group consisting of enzymes, chromophores, fluorochromes, and haptens.

D6

R1.126

~~24~~ 25. (New) The pair of nucleic acid probes of claim ~~23~~ 24, wherein the pair of nucleic acid probes hybridize to a single corresponding nucleic acid molecule.

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R1.126

~~25~~ 26. (New) The pair of nucleic acid probes of claim ~~24~~ 25, wherein the single corresponding nucleic acid molecule is at least a fragment of a chromosome.

R1.126

~~26~~ 27. (New) The pair of nucleic acid probes of claim ~~25~~ 26, wherein the chromosome is not aberrant.

R1.126

~~27~~ 28. (New) The pair of nucleic acid probes of claim ~~21~~ 22 which hybridize *in situ*.

R1.126

~~28~~ 29. (New) The pair of nucleic acid probes of claim ~~27~~ 28, which pair of nucleic acid probes each hybridize *in situ* to only a few linear DNA molecules per cell.